



SEQUENCE LISTING

<110> Michael C. Chen
Chuang-Jiun Chiou
Zhongming Li
Dong-Sheng Chen

<120> COMPOSITIONS AND METHODS FOR TREATING OR
PREVENTING PNEUMOCOCCAL INFECTION

<130> 12844-002001

<140> US 10/702,305

<141> 2003-11-06

<150> US 60/424,497

<151> 2002-11-07

<160> 26

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 471

<212> PRT

<213> Streptococcus pneumoniae

<400> 1

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Met | Ala | Asn | Lys | Ala | Val | Asn | Asp | Phe | Ile | Leu | Ala | Met | Asn | Tyr | Asp | | |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | | | |
| Lys | Lys | Lys | Leu | Leu | Thr | His | Gln | Gly | Glu | Ser | Ile | Glu | Asn | Arg | Phe | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| Ile | Lys | Glu | Gly | Asn | Gln | Leu | Pro | Asp | Glu | Phe | Val | Val | Ile | Glu | Arg | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| Lys | Lys | Arg | Ser | Leu | Ser | Thr | Asn | Thr | Ser | Asp | Ile | Ser | Val | Thr | Ala | | |
| | | 50 | | | | 55 | | | | | 60 | | | | | | |
| Thr | Asn | Asp | Ser | Arg | Leu | Tyr | Pro | Gly | Ala | Leu | Leu | Val | Val | Asp | Glu | | |
| 65 | | | | | 70 | | | | 75 | | | | | 80 | | | |
| Thr | Leu | Leu | Glu | Asn | Asn | Pro | Thr | Leu | Leu | Ala | Val | Asp | Arg | Ala | Pro | | |
| | | | | 85 | | | | 90 | | | | | 95 | | | | |
| Met | Thr | Tyr | Ser | Ile | Asp | Leu | Pro | Gly | Leu | Ala | Ser | Ser | Asp | Ser | Phe | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| Leu | Gln | Val | Glu | Asp | Pro | Ser | Asn | Ser | Ser | Val | Arg | Gly | Ala | Val | Asn | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| Asp | Leu | Leu | Ala | Lys | Trp | His | Gln | Asp | Tyr | Gly | Gln | Val | Asn | Asn | Val | | |
| | | 130 | | | | 135 | | | | | 140 | | | | | | |
| Pro | Ala | Arg | Met | Gln | Tyr | Glu | Lys | Ile | Thr | Ala | His | Ser | Met | Glu | Gln | | |
| 145 | | | | 150 | | | | | 155 | | | | | 160 | | | |
| Leu | Lys | Val | Lys | Phe | Gly | Ser | Asp | Phe | Glu | Lys | Thr | Gly | Asn | Ser | Leu | | |
| | | | 165 | | | | | 170 | | | | 175 | | | | | |
| Asp | Ile | Asp | Phe | Asn | Ser | Val | His | Ser | Gly | Glu | Lys | Gln | Ile | Gln | Ile | | |
| | | 180 | | | | | 185 | | | | | 190 | | | | | |
| Val | Asn | Phe | Lys | Gln | Ile | Tyr | Tyr | Thr | Val | Ser | Val | Asp | Ala | Val | Lys | | |
| | | 195 | | | | 200 | | | | | | 205 | | | | | |
| Asn | Pro | Gly | Asp | Val | Phe | Gln | Asp | Thr | Val | Thr | Val | Glu | Asp | Leu | Lys | | |
| | | 210 | | | | 215 | | | | | | 220 | | | | | |

Gln Arg Gly Ile Ser Ala Glu Arg Pro Leu Val Tyr Ile Ser Ser Val
 225 230 235 240
 Ala Tyr Gly Arg Gln Val Tyr Leu Lys Leu Glu Thr Thr Ser Lys Ser
 245 250 255
 Asp Glu Val Glu Ala Ala Phe Glu Ala Leu Ile Lys Gly Val Lys Val
 260 265 270
 Ala Pro Gln Thr Glu Trp Lys Gln Ile Leu Asp Asn Thr Glu Val Lys
 275 280 285
 Ala Val Ile Leu Gly Gly Asp Pro Ser Ser Gly Ala Arg Val Val Thr
 290 295 300
 Gly Lys Val Asp Met Val Glu Asp Leu Ile Gln Glu Gly Ser Arg Phe
 305 310 315 320
 Thr Ala Asp His Pro Gly Leu Pro Ile Ser Tyr Thr Thr Ser Phe Leu
 325 330 335
 Arg Asp Asn Val Val Ala Thr Phe Gln Asn Ser Thr Asp Tyr Val Glu
 340 345 350
 Thr Lys Val Thr Ala Tyr Arg Asn Gly Asp Leu Leu Leu Asp His Ser
 355 360 365
 Gly Ala Tyr Val Ala Gln Tyr Tyr Ile Thr Trp Asn Glu Leu Ser Tyr
 370 375 380
 Asp His Gln Gly Lys Glu Val Leu Thr Pro Lys Ala Trp Asp Arg Asn
 385 390 395 400
 Gly Gln Asp Leu Thr Ala His Phe Thr Thr Ser Ile Pro Leu Lys Gly
 405 410 415
 Asn Val Arg Asn Leu Ser Val Lys Ile Arg Glu Cys Thr Gly Leu Ala
 420 425 430
 Trp Glu Trp Trp Arg Thr Val Tyr Glu Lys Thr Asp Leu Pro Leu Val
 435 440 445
 Arg Lys Arg Thr Ile Ser Ile Trp Gly Thr Thr Leu Tyr Pro Gln Val
 450 455 460
 Glu Asp Lys Val Glu Asn Asp
 465 470

<210> 2
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 2
 gactagatct ccatatggca aataaagcag taaatgac

38

<210> 3
 <211> 34
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 3
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34

<210> 4
 <211> 38

<212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 4
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 <210> 5
 <211> 36
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 5
 gactggatcc ttactagaga gttgttcccc aaatag 36

 <210> 6
 <211> 35
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 6
 gactggatcc ttactaatct tctacctgag gatag 35

 <210> 7
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 7
 gactggatcc ttactattct accttatctt ctacctgag 39

 <210> 8
 <211> 42
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 8
 gactggatcc ttactaattt tctaccttat cttctacctg ag 42

 <210> 9
 <211> 1413
 <212> DNA
 <213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 9

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| atggcaaata | aagcagtaaa | tgactttata | ctagctatga | attacgataa | aaagaaactc | 60 |
| ttgacccatc | agggagaaaag | tattgaaaat | cgtttcatca | aagagggtaa | tcagctaccc | 120 |
| gatgagtttg | ttgttatcga | aagaaagaag | cggagcttgt | cgacaaatac | aagtgatatt | 180 |
| tctgtaacag | ctaccaacga | cagtcgcctc | tatcctggag | cacttctcgt | agtggatgag | 240 |
| accttgtttag | agaataatcc | cactcttctt | gcggtcgatc | gtgctccgat | gacttatagt | 300 |
| attgatttgc | ctggtttggc | aagtagcgat | agctttctcc | aagtggaaga | cccagcaat | 360 |
| tcaagtgttc | tcggagcggg | aaacgatttg | ttggctaagt | ggcatcaaga | ttatggtcag | 420 |
| gtcaataatg | tcccagctag | aatgcagtat | gaaaaaatca | cggctcacag | catggaacaa | 480 |
| ctcaagggtca | agtttggttc | tgactttgaa | aagacaggga | attctcttga | tattgatttt | 540 |
| aactctgtcc | attcaggcga | aaagcagatt | cagattgtta | attttaagca | gatttattat | 600 |
| acagtcagcg | tagatgctgt | taaaaatcca | ggagatgtgt | ttcaagatac | tgtaacggta | 660 |
| gaggatttaa | aacagagagg | aattttctgca | gagcgtcctt | tggtctatat | ttcgagtgtt | 720 |
| gcttatgggc | gccaagtcta | tctcaagttg | gaaaccacga | gtaagagtga | tgaagtagag | 780 |
| gctgcttttg | aagctttgat | aaaaggagtc | aaggtagctc | ctcagacaga | gtggaaacag | 840 |
| attttgagca | atacagaagt | gaaggcgggt | attttagggg | gcgacccaag | ttcgggtgcc | 900 |
| cgagttgtaa | caggcaaggt | ggatatggta | gaggacttga | ttcaagaagg | cagtcgcttt | 960 |
| acagcagatc | atccaggctt | gccgatttcc | tatacaactt | ctttttttacg | tgacaatgta | 1020 |
| gttgcgacct | ttcaaaatag | tacagactat | gttgagacta | aggttacagc | ttacagaaac | 1080 |
| ggagatttac | tgctggatca | tagtgggtgcc | tatgttgccc | aatattatat | tacttggaat | 1140 |
| gaattatcct | atgatcatca | aggttaaggaa | gtcttgactc | ctaaggcttg | ggacagaaat | 1200 |
| gggcaggatt | taacggctca | ctttaccact | agtattcctt | taaaagggaa | tgttcgtaat | 1260 |
| ctctctgtca | aaattagaga | gcgttcgggg | cttgccctggg | aatgggtggcg | tacggtttat | 1320 |
| gaaaaaacgg | atttgccact | agtgcgtaag | cggacgattt | ctatttgggg | aacaactctc | 1380 |
| tatcctcagg | tagaagataa | ggtagaaaat | gac | | | 1413 |

<210> 10

<211> 1380

<212> DNA

<213> Artificial Sequence

<220>

<223> synthetically generated construct

<400> 10

| | | | | | | |
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| atggcaaata | aagcagtaaa | tgactttata | ctagctatga | attacgataa | aaagaaactc | 60 |
| ttgacccatc | agggagaaaag | tattgaaaat | cgtttcatca | aagagggtaa | tcagctaccc | 120 |
| gatgagtttg | ttgttatcga | aagaaagaag | cggagcttgt | cgacaaatac | aagtgatatt | 180 |
| tctgtaacag | ctaccaacga | cagtcgcctc | tatcctggag | cacttctcgt | agtggatgag | 240 |
| accttgtttag | agaataatcc | cactcttctt | gcggtcgatc | gtgctccgat | gacttatagt | 300 |
| attgatttgc | ctggtttggc | aagtagcgat | agctttctcc | aagtggaaga | cccagcaat | 360 |
| tcaagtgttc | tcggagcggg | aaacgatttg | ttggctaagt | ggcatcaaga | ttatggtcag | 420 |
| gtcaataatg | tcccagctag | aatgcagtat | gaaaaaatca | cggctcacag | catggaacaa | 480 |
| ctcaagggtca | agtttggttc | tgactttgaa | aagacaggga | attctcttga | tattgatttt | 540 |
| aactctgtcc | attcaggcga | aaagcagatt | cagattgtta | attttaagca | gatttattat | 600 |
| acagtcagcg | tagatgctgt | taaaaatcca | ggagatgtgt | ttcaagatac | tgtaacggta | 660 |
| gaggatttaa | aacagagagg | aattttctgca | gagcgtcctt | tggtctatat | ttcgagtgtt | 720 |
| gcttatgggc | gccaagtcta | tctcaagttg | gaaaccacga | gtaagagtga | tgaagtagag | 780 |
| gctgcttttg | aagctttgat | aaaaggagtc | aaggtagctc | ctcagacaga | gtggaaacag | 840 |
| attttgagca | atacagaagt | gaaggcgggt | attttagggg | gcgacccaag | ttcgggtgcc | 900 |
| cgagttgtaa | caggcaaggt | ggatatggta | gaggacttga | ttcaagaagg | cagtcgcttt | 960 |
| acagcagatc | atccaggctt | gccgatttcc | tatacaactt | ctttttttacg | tgacaatgta | 1020 |
| gttgcgacct | ttcaaaatag | tacagactat | gttgagacta | aggttacagc | ttacagaaac | 1080 |

| | | | | | | |
|-------------|------------|------------|-------------|------------|------------|------|
| ggagattttac | tgctggatca | tagtggtgcc | tatgttgccc | aatattatat | tacttggaat | 1140 |
| gaattatcct | atgatcatca | aggtaaggaa | gtcttgactc | ctaaggcttg | ggacagaaat | 1200 |
| gggcaggatt | taacggctca | ctttaccact | agtattcctt | taaaaggga | tggtcgtaat | 1260 |
| ctctctgtca | aaattagaga | gcgttcggg | cttgccctggg | aatggtggcg | tacggtttat | 1320 |
| gaaaaaacg | atttgccact | agtgcgtaag | cggacgattt | ctatttgagg | aacaactctc | 1380 |

<210> 11

<211> 42

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 11

gactaagctt gccaccatgg aaattaatgt gagtaaatta ag

42

<210> 12

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 12

ctgactcgag ttattttact gtaatcaagc catc

34

<210> 13

<211> 954

<212> DNA

<213> Artificial Sequence

<220>

<223> pSA-59 Aly insert

<400> 13

| | | | | | | |
|------------|------------|------------|-------------|------------|------------|-----|
| atggaaatta | atgtgagtaa | attaagaaca | gatttgccctc | aagttggcgt | gcaaccatat | 60 |
| aggcaagtac | acgcacactc | aactgggaat | ccgcattcaa | ccgtacagaa | tgaagcggat | 120 |
| tatcattggc | ggaaagaccc | agaattaggt | tttttctcgc | acattgttgg | gaacggatgc | 180 |
| atcatgcagg | taggacctgt | taataatggt | gcctgggacg | ttgggggagg | ttggaatgct | 240 |
| gagacctatg | cagcgggtga | actgattgaa | agccattcaa | ctaaagaaga | gttcatgacg | 300 |
| gactaccgcc | tttatatcga | actcttacgc | aatctagcag | atgaagcagg | tttgccgaaa | 360 |
| acgcttgata | cagggagttt | agctggaatt | aaaacgcacg | agtattgcac | gaataaccaa | 420 |
| ccaaacaacc | actcagacca | tgtggatcca | tacccttact | tggcaaaatg | gggcattagc | 480 |
| cgtgagcagt | ttaagcatga | tattgagaac | ggcttgacga | ttgaaacagg | ctggcagaag | 540 |
| aatgacactg | gctactggta | cgtacattca | gacggctctt | atccaaaaga | caagtttgag | 600 |
| aaaatcaatg | gcacttggtg | ctactttgac | agttcaggct | atatgcttgc | agaccgctgg | 660 |
| aggaagcaca | cagacggcaa | ttggtactac | tttgaccaat | caggcgaaat | ggctacaggc | 720 |
| tggaagaaaa | tcgctgagaa | gtggtactat | ttcaacgaag | aaggtgccat | gaagacaggc | 780 |
| tgggtcaagt | acaaggacac | ttggtactac | ttagacgcta | aagaaggcgc | aatggtatca | 840 |
| aatgccttta | tccagtcagc | ggacggaaca | ggctggtact | acctcaaacc | agacggaaca | 900 |
| ctggcagaca | agccagaatt | cacagtagag | ccagatggct | tgattacagt | aaaa | 954 |

<210> 14

<211> 318

<212> PRT

<213> Artificial Sequence

<220>

<223> polypeptide of pSA-59 Aly insert sequence

<400> 14

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Met Glu Ile Asn Val Ser Lys Leu Arg Thr Asp Leu Pro Gln Val Gly
 1           5           10           15
Val Gln Pro Tyr Arg Gln Val His Ala His Ser Thr Gly Asn Pro His
          20           25           30
Ser Thr Val Gln Asn Glu Ala Asp Tyr His Trp Arg Lys Asp Pro Glu
          35           40           45
Leu Gly Phe Phe Ser His Ile Val Gly Asn Gly Cys Ile Met Gln Val
          50           55           60
Gly Pro Val Asn Asn Gly Ala Trp Asp Val Gly Gly Gly Trp Asn Ala
65           70           75           80
Glu Thr Tyr Ala Ala Val Glu Leu Ile Glu Ser His Ser Thr Lys Glu
          85           90           95
Glu Phe Met Thr Asp Tyr Arg Leu Tyr Ile Glu Leu Leu Arg Asn Leu
          100          105          110
Ala Asp Glu Ala Gly Leu Pro Lys Thr Leu Asp Thr Gly Ser Leu Ala
          115          120          125
Gly Ile Lys Thr His Glu Tyr Cys Thr Asn Asn Gln Pro Asn Asn His
          130          135          140
Ser Asp His Val Asp Pro Tyr Pro Tyr Leu Ala Lys Trp Gly Ile Ser
145          150          155          160
Arg Glu Gln Phe Lys His Asp Ile Glu Asn Gly Leu Thr Ile Glu Thr
          165          170          175
Gly Trp Gln Lys Asn Asp Thr Gly Tyr Trp Tyr Val His Ser Asp Gly
          180          185          190
Ser Tyr Pro Lys Asp Lys Phe Glu Lys Ile Asn Gly Thr Trp Tyr Tyr
          195          200          205
Phe Asp Ser Ser Gly Tyr Met Leu Ala Asp Arg Trp Arg Lys His Thr
          210          215          220
Asp Gly Asn Trp Tyr Tyr Phe Asp Gln Ser Gly Glu Met Ala Thr Gly
225          230          235          240
Trp Lys Lys Ile Ala Glu Lys Trp Tyr Tyr Phe Asn Glu Glu Gly Ala
          245          250          255
Met Lys Thr Gly Trp Val Lys Tyr Lys Asp Thr Trp Tyr Tyr Leu Asp
          260          265          270
Ala Lys Glu Gly Ala Met Val Ser Asn Ala Phe Ile Gln Ser Ala Asp
          275          280          285
Gly Thr Gly Trp Tyr Tyr Leu Lys Pro Asp Gly Thr Leu Ala Asp Lys
          290          295          300
Pro Glu Phe Thr Val Glu Pro Asp Gly Leu Ile Thr Val Lys
305          310          315

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<210> 15

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> primer

<400> 15

gactaagctt gccaccatgg aagaagctcc cgtagctagt cag

<210> 16
 <211> 37
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> primer

<400> 16
 gactctcgag ctatccatca gggcctaact cattaag

37

<210> 17
 <211> 1377
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> pSA-60 PspA insert

<400> 17
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 aaaaaatctg aagctgctaa gaaggcttac gaagaagcta aaaagaaagc agaagacgct 120
 cagaaaaaat atgatgagga tcagaagaaa actgaggcaa aagcggataa ggaagcaaaa 180
 gcatctgcgg aaatagataa agccacgttt gctgtacaaa gtgcgtatgt aaaattttta 240
 aatgtccaat ctaatcgtca aatttcggag aatgaacgaa aaaaacaatt agcagaaata 300
 gataaagaga tagagaatgc taaacaaaat ttacagaata aacaggaaga atttaataag 360
 gtttagagcag aagtaattcc tgaagcaaag gggtttagctg ttactaaaca aaaagcggaa 420
 gaagctaaaa aagaagcaga agtagctaag agaaaatatg attatgcaac tctaaaggta 480
 gcactagcga agaaagaagt agaggctaag gaacttgaaa ttgaaaaact tcaatatgaa 540
 atttctactt tggaacaaga agttgctatt gctcaacatc aagtagataa tttgaaaaaa 600
 cttcttgctg gtgcggatcc tgatgatggc acaaaagtta tagaagctaa attaaacaaa 660
 ggagaagctg agctaaacgc taaacaagct gagttagcaa aaaaacaaac agaacttgaa 720
 aaacttcttg acagccttga tcctgaagggt aagactcagg atgaattaga taaagaagct 780
 gctgaagctg agttggataa aaaagctgat gaacttcaaa ataaagttgc tgatttagaa 840
 aaaggaattg ctctttatca aatcaaagtc gctgaattaa ataaagaaat tgctagactt 900
 caaagcgatt taaaagatgc tgaagaaaat aatgtagaag actatattaa agaaggttta 960
 gagcaagcta tcgctgataa aaaagctgaa ttagctacaa ctcaacaaaa catagataaa 1020
 actcaaaaag atttagagga tgctgaatta gaacttgaaa aagtagtagc tacattagac 1080
 cctgaaggta aaactcaaga tgaattagat aaagaagctg cagaagatgc taatattgaa 1140
 gctcttcaaa acaaagttgc tgatctagaa aacaagggtg ctgaattaga taaagaagtt 1200
 actagacttc aaagcgattt aaaagatgct gaagaaaaca atgtagaaga ctacgttaaa 1260
 gaaggcttag ataaagctct tactgataaa aaagttgaat taaataatac tcaaaaagca 1320
 ttagatactg ctcaaaaagc attagatact gctcttaatg agttaggccc tgatgga 1377

<210> 18
 <211> 459
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> polypeptide of pSA-60 PspA insert sequence

<400> 18
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 1 5 10 15
 Asp Ala Ala Val Lys Lys Ser Glu Ala Ala Lys Lys Ala Tyr Glu Glu

| | | | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| 20 | | | | | | | 25 | | | | | | | 30 | | | | | | | |
| Ala | Lys | Lys | Lys | Ala | Glu | Asp | Ala | Gln | Lys | Lys | Tyr | Asp | Glu | Asp | Gln | | | | | | |
| 35 | | | | | | | 40 | | | | | | | 45 | | | | | | | |
| Lys | Lys | Thr | Glu | Ala | Lys | Ala | Asp | Lys | Glu | Ala | Lys | Ala | Ser | Ala | Glu | | | | | | |
| 50 | | | | | | | 55 | | | | | | | 60 | | | | | | | |
| Ile | Asp | Lys | Ala | Thr | Phe | Ala | Val | Gln | Ser | Ala | Tyr | Val | Lys | Phe | Leu | | | | | | |
| 65 | 70 | | | | | | | 75 | | | | | | | 80 | | | | | | |
| Asn | Val | Gln | Ser | Asn | Arg | Gln | Ile | Ser | Glu | Asn | Glu | Arg | Lys | Lys | Gln | | | | | | |
| 85 | | | | | | | 90 | | | | | | | 95 | | | | | | | |
| Leu | Ala | Glu | Ile | Asp | Lys | Glu | Ile | Glu | Asn | Ala | Lys | Gln | Asn | Leu | Gln | | | | | | |
| 100 | | | | | | | 105 | | | | | | | 110 | | | | | | | |
| Asn | Lys | Gln | Glu | Glu | Phe | Asn | Lys | Val | Arg | Ala | Glu | Val | Ile | Pro | Glu | | | | | | |
| 115 | | | | | | | 120 | | | | | | | 125 | | | | | | | |
| Ala | Lys | Gly | Leu | Ala | Val | Thr | Lys | Gln | Lys | Ala | Glu | Glu | Ala | Lys | Lys | | | | | | |
| 130 | | | | | | | 135 | | | | | | | 140 | | | | | | | |
| Glu | Ala | Glu | Val | Ala | Lys | Arg | Lys | Tyr | Asp | Tyr | Ala | Thr | Leu | Lys | Val | | | | | | |
| 145 | 150 | | | | | | | 155 | | | | | | | 160 | | | | | | |
| Ala | Leu | Ala | Lys | Lys | Glu | Val | Glu | Ala | Lys | Glu | Leu | Glu | Ile | Glu | Lys | | | | | | |
| 165 | | | | | | | 170 | | | | | | | 175 | | | | | | | |
| Leu | Gln | Tyr | Glu | Ile | Ser | Thr | Leu | Glu | Gln | Glu | Val | Ala | Ile | Ala | Gln | | | | | | |
| 180 | | | | | | | 185 | | | | | | | 190 | | | | | | | |
| His | Gln | Val | Asp | Asn | Leu | Lys | Lys | Leu | Leu | Ala | Gly | Ala | Asp | Pro | Asp | | | | | | |
| 195 | | | | | | | 200 | | | | | | | 205 | | | | | | | |
| Asp | Gly | Thr | Lys | Val | Ile | Glu | Ala | Lys | Leu | Asn | Lys | Gly | Glu | Ala | Glu | | | | | | |
| 210 | | | | | | | 215 | | | | | | | 220 | | | | | | | |
| Leu | Asn | Ala | Lys | Gln | Ala | Glu | Leu | Ala | Lys | Lys | Gln | Thr | Glu | Leu | Glu | | | | | | |
| 225 | 230 | | | | | | | 235 | | | | | | | 240 | | | | | | |
| Lys | Leu | Leu | Asp | Ser | Leu | Asp | Pro | Glu | Gly | Lys | Thr | Gln | Asp | Glu | Leu | | | | | | |
| 245 | | | | | | | 250 | | | | | | | 255 | | | | | | | |
| Asp | Lys | Glu | Ala | Ala | Glu | Ala | Glu | Leu | Asp | Lys | Lys | Ala | Asp | Glu | Leu | | | | | | |
| 260 | | | | | | | 265 | | | | | | | 270 | | | | | | | |
| Gln | Asn | Lys | Val | Ala | Asp | Leu | Glu | Lys | Gly | Ile | Ala | Pro | Tyr | Gln | Ile | | | | | | |
| 275 | | | | | | | 280 | | | | | | | 285 | | | | | | | |
| Lys | Val | Ala | Glu | Leu | Asn | Lys | Glu | Ile | Ala | Arg | Leu | Gln | Ser | Asp | Leu | | | | | | |
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| Lys | Asp | Ala | Glu | Glu | Asn | Asn | Val | Glu | Asp | Tyr | Ile | Lys | Glu | Gly | Leu | | | | | | |
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| Glu | Gln | Ala | Ile | Ala | Asp | Lys | Lys | Ala | Glu | Leu | Ala | Thr | Thr | Gln | Gln | | | | | | |
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| Asn | Ile | Asp | Lys | Thr | Gln | Lys | Asp | Leu | Glu | Asp | Ala | Glu | Leu | Glu | Leu | | | | | | |
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| Glu | Lys | Val | Leu | Ala | Thr | Leu | Asp | Pro | Glu | Gly | Lys | Thr | Gln | Asp | Glu | | | | | | |
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| Lys | Val | Ala | Asp | Leu | Glu | Asn | Lys | Val | Ala | Glu | Leu | Asp | Lys | Glu | Val | | | | | | |
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| Thr | Arg | Leu | Gln | Ser | Asp | Leu | Lys | Asp | Ala | Glu | Glu | Asn | Asn | Val | Glu | | | | | | |
| 405 | | | | | | | 410 | | | | | | | 415 | | | | | | | |
| Asp | Tyr | Val | Lys | Glu | Gly | Leu | Asp | Lys | Ala | Leu | Thr | Asp | Lys | Lys | Val | | | | | | |
| 420 | | | | | | | 425 | | | | | | | 430 | | | | | | | |
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| Asp | Thr | Ala | Leu | Asn | Glu | Leu | Gly | Pro | Asp | Gly | | | | | | | | | | | |
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